

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/580,877
Source: IFWP
Date Processed by STIC: 06/19/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/19/2006

PATENT APPLICATION: US/10/580,877

TIME: 11:11:36

Input Set : A:\Sequence Listing (diskette).txt

Output Set: N:\CRF4\06192006\J580877.raw

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3 <110> APPLICANT: DOI, Hirofumi
4     MASUDA, Shoichi
5     ISUMI, Yoshitaka
7 <120> TITLE OF INVENTION: Procaspase 1 Activation Inhibitor
9 <130> FILE REFERENCE: 3190-097
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/580,877
12 <141> CURRENT FILING DATE: 2006-05-25
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/017586
15 <151> PRIOR FILING DATE: 2004-11-26
17 <150> PRIOR APPLICATION NUMBER: JP P2003-396278
18 <151> PRIOR FILING DATE: 2003-11-26
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.1
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25 <211> LENGTH: 3120
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(3120)
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37 gct ttt cag gca cag agg agc cag ctg gtc gag ctg ctg gtc tca ggg     144
38 tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg ctg ctg tcc tgg gag     192
39 gtc ctc tcc tgg gag gac tac gag ggc ttc cac ctc ctg ggc cag cct     240
40 ctc tcc cac ttg gcc agg cgc ctt ctg gac acc gtc tgg aat aag ggt     288
41 act tgg gcc tgt cag aag ctc atc gcg gct gcc caa gaa gcc cag gcc     336
42 gac agc cag tcc ccc aag ctg cat ggc tgc tgg gac ccc cac tcg ctc     384
43 cac cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg     432
44 ctc cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt     480
45 ttc gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca     528
47 ccg tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg     576
48 aat gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc     624
49 cca ttg gcc ctg cct ttg gaa gct gcc aca tgc aag aag tat atg gcc     672
50 aag ctg agg acc acg gtg tct gct cag tct cgc ttc ctc agt acc tat     720
51 gat gga gca gag acg ctc tgc ctg gag gac ata tac aca gag aat gtc     768
52 ctg gag gtc tgg gca gat gtg ggc atg gct gga ccc ccg cag aag agc     816
53 cca gcc acc ctg ggc ctg gag gag ctc ttc agc acc cct ggc cac ctc     864
54 aat gac gat gcg gac act gtg ctg gtg gtg ggt gag gcg ggc agt ggc     912
55 aag agc acg ctc ctg cag cgg ctg cac ttg ctg tgg gct gca ggg caa     960
56 gac ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg    1008
57 cag tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac    1056

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63 ttc ctc agg aag tac atc cgc acc gag ttc aac ctc aag ggc ttc tct      1344
64 gaa cag ggc atc gag ctg tac ctg agg aag cgc cat cat gag ccc ggg      1392
65 gtg gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca gcc ctg cac      1440
66 ggt ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc aaa tgc cac      1488
67 cag gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc act aca gat      1536
68 atg tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc acc ccc cca      1584
69 gac tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg ggc cgc ctc      1632
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72 cct gat gac att tct ctt ggc ttc ctg gtg cgt gcc aaa ggt gtc gtg      1776
73 cca ggg agt acg gcg ccc ctg gaa ttc ctt cac atc act ttc cag tgc      1824
74 ttc ttt gcc gcg ttc tac ctg gca ctc agt gct gat gtg cca cca gct      1872
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76 gcc agg ctc ctg ccc acg atg tgc atc cag gcc tgc gag gga aag gac      1968
77 agc agc gtg gca gct ttg ctg cag aag gcc gag ccg cac aac ctt cag      2016
78 atc aca gca gcc ttc ctg gca ggg ctg ttg tcc cgg gag cac tgg ggc      2064
79 ctg ctg gct gag tgc cag aca tct gag aag gcc ctg ctc cgg cgc cag      2112
80 gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc cgc aag cac ttc cac      2160
81 tcc atc ccg cca gct gca ccg ggt gag gcc aag agc gtg cat gcc atg      2208
82 ccc ggg ttc atc tgg ctc atc cgg agc ctg tac gag atg cag gag gag      2256
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84 ttg aca ttt tgc agt gtg ggc ccc act gag tgt gct gcc ctg gcc ttt      2352
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86 tct gtg ggt gac att ggc gtg gag cag ctg ctg cct tgc ctt ggt gtc      2448
87 tgc aag gct ctg tat ttg cgc gat aac aat atc tca gac cga ggc atc      2496
88 tgc aag ctc att gaa tgt gct ctt cac tgc gag caa ttg cag aag tta      2544
89 gct cta ttc aac aac aaa ttg act gag ggc tgt gca cac tcc atg gct      2592
90 aag ctc ctt gca tgc agg cag aac ttc ttg gca ttg agg ctg ggg aat      2640
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92 ggc aac acc tcc ttg cag ttc ctg gga ttc tgg ggc aac aga gtg ggt      2736
93 gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat cac cag agc      2784
94 ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt gtg ggt gcc      2832
95 caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta gaa gaa ctc      2880
96 tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt tct ctc gca      2928
97 gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aag ttg tcc aat      2976
98 aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa      3024
99 agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc      3069
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103 <210> SEQ ID NO: 2
104 <211> LENGTH: 1040
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 2

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111 1 5 10 15
114 Ser Val Leu Leu Gly His Ser Pro Gly Cys Glu Met Cys Ser Gln Glu
115 20 25 30
118 Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu Leu Leu Val Ser Gly
119 35 40 45
122 Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp Leu Leu Ser Trp Glu
123 50 55 60
126 Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His Leu Leu Gly Gln Pro
127 65 70 75 80
130 Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr Val Trp Asn Lys Gly
131 85 90 95
134 Thr Trp Ala Cys Gln Lys Leu Ile Ala Ala Gln Glu Ala Gln Ala
135 100 105 110
138 Asp Ser Gln Ser Pro Lys Leu His Gly Cys Trp Asp Pro His Ser Leu
139 115 120 125
142 His Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg
143 130 135 140
146 Leu His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly
147 145 150 155 160
150 Phe Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr
151 165 170 175
154 Pro Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala
155 180 185 190
158 Asn Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val
159 195 200 205
162 Pro Leu Ala Leu Pro Leu Glu Ala Ala Thr Cys Lys Lys Tyr Met Ala
163 210 215 220
166 Lys Leu Arg Thr Thr Val Ser Ala Gln Ser Arg Phe Leu Ser Thr Tyr
167 225 230 235 240
170 Asp Gly Ala Glu Thr Leu Cys Leu Glu Asp Ile Tyr Thr Glu Asn Val
171 245 250 255
174 Leu Glu Val Trp Ala Asp Val Gly Met Ala Gly Pro Pro Gln Lys Ser
175 260 265 270
178 Pro Ala Thr Leu Gly Leu Glu Glu Leu Phe Ser Thr Pro Gly His Leu
179 275 280 285
182 Asn Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly
183 290 295 300
186 Lys Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln
187 305 310 315 320
190 Asp Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu
191 325 330 335
194 Gln Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His
195 340 345 350
198 Cys Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu
199 355 360 365
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203 370 375 380
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214 Lys Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala
215          420          425          430
218 Phe Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser
219          435          440          445
222 Glu Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly
223          450          455          460
226 Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His
227 465          470          475          480
230 Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His
231          485          490          495
234 Gln Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr Thr Thr Asp
235          500          505          510
238 Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro
239          515          520          525
242 Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu
243          530          535          540
246 Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met
247 545          550          555          560
250 Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser
251          565          570          575
254 Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys Gly Val Val
255          580          585          590
258 Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr Phe Gln Cys
259          595          600          605
262 Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val Pro Pro Ala
263          610          615          620
266 Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn Ser Pro Met
267 625          630          635          640
270 Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu Gly Lys Asp
271          645          650          655
274 Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His Asn Leu Gln
275          660          665          670
278 Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu His Trp Gly
279          675          680          685
282 Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu Arg Arg Gln
283          690          695          700
286 Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys His Phe His
287 705          710          715          720
290 Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val His Ala Met
291          725          730          735
294 Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu
295          740          745          750
298 Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly His Leu Lys
299          755          760          765
302 Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala Leu Ala Phe
303          770          775          780

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315                               820                               825                               830
318 Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu Gln Lys Leu
319                               835                               840                               845
322 Ala Leu Phe Asn Asn Lys Leu Thr Asp Gly Cys Ala His Ser Met Ala
323                               850                               855                               860
326 Lys Leu Leu Ala Cys Arg Gln Asn Phe Leu Ala Leu Arg Leu Gly Asn
327 865                               870                               875                               880
330 Asn Tyr Ile Thr Ala Ala Gly Ala Gln Val Leu Ala Glu Gly Leu Arg
331                               885                               890                               895
334 Gly Asn Thr Ser Leu Gln Phe Leu Gly Phe Trp Gly Asn Arg Val Gly
335                               900                               905                               910
338 Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp His Gln Ser
339                               915                               920                               925
342 Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser Val Gly Ala
343                               930                               935                               940
346 Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu Glu Glu Leu
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350 Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys Ser Leu Ala
351                               965                               970                               975
354 Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Lys Leu Ser Asn
355                               980                               985                               990
358 Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu
359                               995                               1000                               1005
362 Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe
363                               1010                               1015                               1020
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375 <211> LENGTH: 1212
376 <212> TYPE: DNA
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387 agg gtg ctg aac aag gaa gag atg gag aaa gta aaa cgt gaa aat gct 144
388 aca gtt atg gat aag acc cga gct ttg att gac tcc gtt att ccg aaa 192
389 ggg gca cag gca tgc caa att tgc atc aca tac att tgt gaa gaa gac 240
390 agt tac ctg gca ggg acg ctg gga ctc tca gca gat caa aca tct gga 288
391 aat tac ctt aat atg caa gac tct caa gga gta ctt tct tcc ttt cca 336

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number